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Sequence Listing could not be accepted.
If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2008; month=1; day=28; hr=18; min=44; sec=17; ms=808;]
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Reviewer Comments:
<150> Polynucleotides and Polypeptides in Plants
<151> 2003-09-18

The above <150> response is invalid: per Sequence Rules, the only response to <150> can be a prior or related application number, not an invention title.

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<211> 102
<212> PRT
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<223> Figs 6A-6C consensus sequence, where X is any amino acid and the 1st X is is no amino acid or A, P, G, S or T, 2nd X is 0-17 residues, 3rd X is 0-32 residues, 4th X is K, R, N or Q, 5th X is no residue or P, 6th X is V, I, L, M, or A, 7th X is H, Q, N, A, M or C, 8th X is R or K, 9th X is no residue or L, I, M, V, A, or T

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1 5 10 15

Asn Val Ser Arg Ile Met Lys Xaa Ala Leu Pro Ala Asn Ala Lys Ile
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Ser Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile
35 40 45

Ser Phe Ile Thr Xaa Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys
50 55 60

Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu
65 70 75 80

Gly Phe Glu Asp Tyr Xaa Glu Pro Leu Lys Val Tyr Leu Xaa Xaa Tyr
85 90 95

Arg Glu Xaa Glu Gly Glu
100

The above <223> response explaining "<213> Artificial Sequence" is insufficient: please give more information regarding the source of the genetic material. This error also occurs in Sequences 104-105, 107-108, and 113-115. Also, the above <223> response beginning "Figs 6A-6C consensus sequence" exceeds the Sequence Rules' required 72-character limit (this includes white spaces). Please insert hard returns, so that the lines do not exceed 72 characters. Per Sequence Rules, the <223> response has a maximim of 4 lines. If the response exceeds 4 lines, please insert a "<220>" above the 5th line, and insert a "<223>" at the beginning of the 5th line. This error also appears in other sequences.

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Validated By CRFValidator v 1.0.3

Application No: 10675852 Version No: 3.0

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SEQUENCE LISTING

<110> Mendel Biotechnology, Inc.
HEARD, Jacqueline E
KEDDIE, James S
CREELMAN, Robert A
PINEDA, Omaira
JIANG, Cai-Zhong
RATCLIFFE, Oliver
KUMIMOTO, Roderick
GUTTERSON, Neal
SHERMAN, Bradley K

<120> PLANT TRANSCRIPTIONAL REGULATORS OF ABIOTIC STRESS

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<151> 2000-11-16

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<151> 2003-02-25

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cctatagcta atatcagcag gatcatgaag aaagcgttgc ctcctaatgg taagattgga 240

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Arg Ile Met Lys Lys Ala Leu Pro Pro Asn Gly Lys Ile Gly Lys Asp
35 40 45

Ala Lys Asp Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile
50 55 60

Thr Ser Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Val
65 70 75 80

Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Asp
85 90 95

Tyr Leu Glu Pro Leu Lys Ile Tyr Leu Ala Arg Tyr Arg Glu Leu Glu
100 105 110

Gly Asp Asn Lys Gly Ser Gly Lys Ser Gly Asp Gly Ser Asn Arg Asp
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cggacagtcc tccttgtctc caagagagca agacaggttc ttgccgatcg ctaacgtcag 300

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aggttttgag gattatgttg agccattgaa agtttacttg cagaggttta gggagatcga 540

aggggagagg actggactag ggaggccaca gactggtggt gaggtcggag agcatcagag 600

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ctctctctgt atatagatac ataaatacat gtatacacat gcctattttt acgacccata 840

taaggtatct atcatgtgat agaacgaaca ttggtgttgg tgatgtaaaa tcagatgtgc 900

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<213> Arabidopsis thaliana

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Pro Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn
35 40 45

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Ala Lys Ile Ser Lys Asp Ala Lys Glu Thr Met Gln Glu Cys Val Ser
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Glu Phe Ile Ser Phe Val Thr Gly Glu Ala Ser Asp Lys Cys Gln Lys
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Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr
                85                  90                  95

Thr Leu Gly Phe Glu Asp Tyr Val Glu Pro Leu Lys Val Tyr Leu Gln
            100                 105                 110

Arg Phe Arg Glu Ile Glu Gly Glu Arg Thr Gly Leu Gly Arg Pro Gln
        115                 120                 125

Thr Gly Gly Glu Val Gly Glu His Gln Arg Asp Ala Val Gly Asp Gly
    130                 135                 140

Gly Gly Phe Tyr Gly Gly Gly Gly Gly Met Gln Tyr His Gln His His
145                 150                 155                 160

Gln Phe Leu His Gln Gln Asn His Met Tyr Gly Ala Thr Gly Gly Gly
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<212> DNA
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gcgaacgcaa aaatctctaa ggatgctaaa gaaacggttc aagagtgtgt atcggaattc    180

ataagtttca tcaccggtga ggcttctgac aagtgtcaga gagagaagag gaagacaatc    240

aacggtgacg atcttctttg ggcgatgact acgctagggt ttgaggacta cgtggagcct    300

ctcaaggttt atctgcaaaa gtatagggag gtggaaggag agaagactac tacggcaggg    360
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agacaaggcg ataaggaagg tggaggagga ggcggtggag ctggaagtgg aagtggagga 420

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tcttaa 486

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<220>
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20 25 30

Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile Ser Lys Asp
35 40 45

Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile
50 55 60

Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile
65 70 75 80

Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe Glu Asp
85 90 95

Tyr Val Glu Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Val Glu
100 105 110

Gly Glu Lys Thr Thr Thr Ala Gly Arg Gln Gly Asp Lys Glu Gly Gly
115 120 125

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Gly Gly Gly Met Val Thr Thr Met Gly His Gln Phe Ser His His Phe
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agccgtatca tgaaaagagg tcttcctgct aatgggaaaa tcgctaaaga tgctaaggag 180

attgtgcagg aatgtgtctc tgaattcatc agtttcgtca ccagcgaagc gagtgataaa 240

tgtcaaagag agaaaaggaa gactattaat ggagatgatt tgctttgggc aatggctact 300

ttaggatttg aagactacat ggaacctctc aaggtttacc tgatgagata tagagagggt 360

gacacaaagg gatcagcaaa aggtggggat ccaaatgcaa agaaagatgg gcaatcaagc 420

caaaatggcc agttctcgca gcttgctcac caaggtcctt atgggaactc tcaagtaact 480

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<213> Arabidopsis thaliana

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Ser Gly Gly Asp Gln Ser Pro Arg Ser Leu His Val Arg Glu Gln Asp
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Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Arg Gly Leu
35 40 45

Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Ile Val Gln Glu
50 55 60

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Cys Val Ser Glu Phe Ile Ser Phe Val Thr Ser Glu Ala Ser Asp Lys
65                  70                  75                  80

Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp
                85                  90                  95

Ala Met Ala Thr Leu Gly Phe Glu Asp Tyr Met Glu Pro Leu Lys Val
            100                 105                 110

Tyr Leu Met Arg Tyr Arg Glu Gly Asp Thr Lys Gly Ser Ala Lys Gly
        115                 120                 125

Gly Asp Pro Asn Ala Lys Lys Asp Gly Gln Ser Ser Gln Asn Gly Gln
    130                 135                 140

Phe Ser Gln Leu Ala His Gln Gly Pro Tyr Gly Asn Ser Gln Val Thr
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Phe Pro Leu Phe Ser Ser His Ser Ser Asn Thr His His Ser Leu Leu
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caaagagaga aaaggaagac catcaatgga gatgatttgc tttgggctat ggccacttta    300

ggattcgaag attacatcga tcccctcaag gtttacctga tgcgatatag agagatggag    360

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aatctgagtg atccactttc catagatatg gattgtgaag ctatttatca ccacttcatt 660

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Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Arg Gly Leu Pro
35 40 45

Leu Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Met Gln Glu Cys
50 55 60

Val Ser Glu Phe Ile Ser Phe Val Thr Ser Glu Ala Ser Asp Lys Cys
65 70 75 80

Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala
85 90 95

Met Ala Thr Leu Gly Phe Glu Asp Tyr Ile Asp Pro Leu Lys Val Tyr
100 105 110

Leu Met Arg Tyr Arg Glu Met Glu Gly Asp Thr Lys Gly Ser Gly Lys
115 120 125

Gly Gly Glu Ser Ser Ala Lys Arg Asp Gly Gln Pro Ser Gln Val Ser
130 135 140

Gln Phe Ser Gln Val Pro Gln Gln Gly Ser Phe Ser Gln Gly Pro Tyr

145 150 155 160

Gly Asn Ser Gln Ser Leu Arg Phe Gly Asn Ser Ile Glu His Leu Glu
165 170 175

Val Leu Met Ser Ser Thr Arg Thr Leu Phe Ile Thr Ile Phe Arg Asp
180 185 190

Ser Thr Met Pro Val Val Ser Glu Asn Leu Ser Asp Pro Leu Ser Ile
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35 40 45

Lys Ile Ala Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu
50 55 60

Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Asp Lys Cys Gln Arg Glu
65 70 75 80

Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr
85 90 95

Leu Gly Phe Glu Asp Tyr Met Asp Pro Leu Lys Ile Tyr Leu Thr Arg
100 105 110

Tyr Arg Glu Met Glu Gly Asp Thr Lys Gly Ser Ala Lys Gly Gly Asp
115 120 125

Ser Ser Ala Lys Arg Asp Val Gln Pro Ser Pro Asn Ala Gln Leu Ala

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His Gln Gly Ser Phe Ser Gln Asn Val Thr Tyr Pro Asn Ser Gln Gly
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Arg His Met Met Val Pro Met Gln Gly Pro Glu
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